

SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> New nucleotide sequences which code for the luxS gene

<130> 000457 BT

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10 <141>

<160> 4

<170> PatentIn Ver. 2.1

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<210> 1

<211> 1902

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (342)..(1610)

<223> luxS gene

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cggtgcgttc gaccgcgggc atcgcgtcga tgggaaggcc gtcagtaatt acttcggggg 180

ctgcctcggg ggtggtctct ggggttgctt caggttcgc cggggtacaa gcggtgagca 240

35

tgatggaagc agcgaggata gtaggtaatg tacgacgcac gcagtcaagc ctagatcgtg 300

tgtcggaaac cggaacgaat gagctcgatg ttgaaacct t gtg aag aag ggg aat 356
Met Lys Lys Gly Asn
1 5

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caa ccg ggc gcg atg agc tat cgc aac agt atc cac att ttg aca gcc 404
Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile His Ile Leu Thr Ala

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tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc cgc ctg acg ctg ccg 452
Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro

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atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg tgg ggt ttt ctg tac 500
Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val Trp Gly Phe Leu Tyr

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55

ttc tat gga tca acc aaa cgc gta gat ttg agc cac ggc atg cag ctg 548
Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser His Gly Met Gln Leu

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ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att ttt atg gtg ccg atc 596
Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile Phe Met Val Pro Ile

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	gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg ttt ttc ctc tat cta	644
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5	cag gtg atg cct gac gtg aga ggc att att gcg att ttg ggt gcg aca	692
	Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr	
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10	gcg att gcg att gcc agc cag tat tcc gtg ggg ttg acc ttt ggt ggt	740
	Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly	
	120 125 130	
15	gtg atg ggt ccg gtg gtc tct gcg atc gtg acc gtg gct att gat tac	788
	Val Met Gly Pro Val Val Ser Ala Ile Val Thr Val Ala Ile Asp Tyr	
	135 140 145	
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	Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu Lys Gln Glu Leu Ile	
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	gat cag ttg att gaa act cgc tcc cag ctg gcg gtg acg gaa cga aat	884
	Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala Val Thr Glu Arg Asn	
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	Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala His Glu Ile His Asp	
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	Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met Leu Leu His Val Ser	
	200 205 210	
35	gaa cag gag att ctc gtt gct gag atg gaa gag aag cca aag gag gcg	1028
	Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu Lys Pro Lys Glu Ala	
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40	atc gtg aag aag atg cgc ctt gcc cga caa aca gcc tcc gac aat ctc	1076
	Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu	
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	agt gag gct cgc gcg atg att gcg gcg ttg caa ccg gca gcg ctg tct	1124
	Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser	
	250 255 260	
45	aaa acc tcc ttg gaa gca gca ctt cac cgc gtc aca gaa ccg ttg ttg	1172
	Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val Thr Glu Pro Leu Leu	
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	Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp Val Arg Gln Leu Pro	
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55	atg aaa act gaa gcc acc ctt ctg cga att gct caa ggt gcg atc gga	1268
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aat gtg gcg aaa cat tca gag gcg aaa aac tgc cac gtg aca cta acc 1316
 Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys His Val Thr Leu Thr
 310 315 320 325

5 tac gaa gac aca gaa gta cgc ctt gat gtg gtt gat gac ggt gtg ggt 1364
 Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val Asp Asp Gly Val Gly
 330 335 340

10 ttt gag cct tcg gaa gtg tcc agt acc ccc gct ggc ctt ggc cat atc 1412
 Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala Gly Leu Gly His Ile
 345 350 355

15 ggc tta acc gca ttg cag cag cgt gcg atg gaa ttg cac ggc gaa gtt 1460
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20 ata gtg gaa tct gca tat ggg cag ggt act gcg gta tct gca gca ttg 1508
 Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala Val Ser Ala Ala Leu
 375 380 385

ccg gtg gag cca cca gag ggg ttt gtc ggg gcg ccg gtt ttg gca gat 1556
 Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala Pro Val Leu Ala Asp
 390 395 400 405

25 tcg gac tca agt gct aca ggc gag gtt gaa cta agt tct cca act gac 1604
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30 gat gag taaggctaga ctaaagtacg attcatctgc tcatcgatac tcttgaaggc 1660
 Asp Glu

gcatttttcat tcgaaacgaa gtgcgccatt gggaaggacc tagttcaaac aatgattcgc 1720

35 gtgctgcttg ctgatgacca cgaaatcgtg aggctcggac tccgagctgt gctggaaagc 1780

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40 ac 1902

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55 Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val
 35 40 45

Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser
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His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile
 65 70 75 80
 5 Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu
 85 90 95
 Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala
 100 105 110
 10 Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly
 115 120 125
 Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr
 130 135 140
 15 Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu
 145 150 155 160
 20 Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala
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 25 His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met
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 30 Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr
 225 230 235 240
 35 Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln
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 Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
 260 265 270
 40 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
 275 280 285
 Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala
 290 295 300
 45 Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys
 305 310 315 320
 50 His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val
 325 330 335
 Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala
 340 345 350
 55 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
 355 360 365

Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
 370 375 380

5 Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala
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